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SEARCH REQUEST FORM

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Requester's Full Name: _____ Examiner # : _____ Date: _____

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Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.
****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____ _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

****

STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher: _____ (am)	NA Sequence (#)___ ✓	STN _____
Searcher Phone #: __22509	AA Sequence (#)___ ✓	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: __8|3	Bibliographic _____	Dr.Link _____
Date Completed: __8|10	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: ____	Fulltext _____	Sequence Systems __ ✓
Clerical Prep Time: ____ 20	Patent Family _____	WWW/Internet _____
Online Time: ____ +20	Other _____	Other (specify)_____

PTO-1590 (8-01)

RESULT 6
ID 002838
AC 002838;
002838;
PRELIMINARY;
PRT; 325 AA.

DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD86.
GN B7-2.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97047772; PubMed=8892613;
RA Maher S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,
RA Bothwell A.L.;
RT "Porcine endothelial CD86 is a major costimulator of xenogeneic human
RT T cells: cloning, sequencing, and functional expression in human
RT endothelial cells.";
RL J. Immunol. 157:3838-3844(1996).
DR EMBL; L76099; AAB61307.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 325 AA; 36527 MW; 988BE08137B0597D CRC64;

US-10-790-396-9 (1-987) x 002838 (1-325)

Alignment Scores:
Pred. No.:
Score: 1199.00   Length: 325
Percent Similarity: 82.42%   Matches: 239
Best Local Similarity: 72.42%   Conservative: 33
Query Match: 68.63%   Mismatches: 46
DB: 6   Indels: 12
                                             Gaps: 7

Qy   19 ATGGAACTGAATAACATTCTCTTTGTGATGACCCTCGTTGCTCTTATGGTGTGCTTCCATG 78
         ||| ||||||||||||||| ||| :::|||||||
Db   1 MetGlyLeuLeuSerHisThrLeuLeuPheValMetAlaLeuLeuLeuSerGlyAlaLeuSerLeu 20

Qy   79 AAGAGTCAGCATATTTCAACAAGACTGGAGAACTGCCATGCCAGTTTACAAAATTCTCAA 138
Db   21 LysSerGlnAlaTyrPheAsnLysThrGlyGluLeuProCysHisPheThrAsnSerGln 40

Qy 139 AACATAAAGCCTGGAATGAAGTTGGAGTGTTGGGCAGGACCAGGATAAGCTCGGTTCGTAC 198
Db   41 AsnLeuSerLeuAspGluLeuValIleLePheThrTrpGlnAspGlnAsnLeuValLeuTyr 60

Qy 199 GAGCTATACAGAGGCCAAAGAGAACCCTCAAAATGTTCATCGAAGTATAAGGGCCGCACA 258
Db   61 GluLeuTyrArgGlyGlnInGluLysProHisAsnValIleProGlnLeuTyrArgThr 80

Qy 259 AGCTTTGACAAAGACATATTCAACAAGACTGGAGAACTCCATAATATTCAGATCAAGGAGC 318
Db   81 SerPheAspLysInAlaThrTrpThrLeuArgLeuHisAsnValGlnIleLysLysAspGlyGly 100

Qy 319 TTGTATCAAAGTTTCGTTCATCATAAAGGCCGCAAAGACTCGGTTCCCATGCCACCAGATG 378
Db 101 SerTyrGlnCysPheIleHisHisLysGlyProSerHisGluCys 120

Qy 379 AATTCTGACCTATCAGTGCTTGCTAACTTCAGTCAACCTGAAAATAATGGTAACTTCTAAT 438
Db 121 SerSerAspLeuSerLeuAlaAsnPheSerGlnProGluIleAsnLeuLeuThrAsn 140

Qy 439 AGAACAGAAAATTCTCGGCCATCATAAAATTGACCTGCTCATCATACAAGGTTACCCAGAA 498
Db 141 HisThrGluAsnSer---ValIleAsnLeuLeuThrCysSerSerThrGlyIleTyrProGlu 159

Qy 499 CCCAAGGAGATCTGTATTTTTGGTAAAAACCGAGAATTCAAGTACTAAGGTATGTAACTTC 558
Db 160 ProGlnArgMetTyrMetLeuLeuAsnThrLysAsnSerThrThrGlnHisAspAlaAsp 179

Qy 559 ATGAAGAAATCTCAAAATAATGTCACAGAACTCTACAACGTTTCTATCAGCTTGTCCTTC 618
         ||||||||||||| |||:: |||| :::|||
Db 160 ...

─────────────────────────────

Qy   16 ACTATGGAACTGAATAACATTCTCTTTGTGATGACCCTCGTTGCTCTTCC 75
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Db   7 ThrMetGlyLeuSerHisThrLeuLeuValMetAlaLeuLeuLeuSerGlyValSerSer 26

Qy   76 ATGGAGAGTCAGCATATTTCAACAAGACTGGAGAACTGCCATGCCAGTTTACAAAATCT 135
Db   27 MetLysSerGlnAlaTyrPheAsnLysThrGlyGluLeuProCysHisPheThrAsnSer 46

Qy 136 CAAAACATAAAGCCTGGAATGAAGTTGGAGTGTTTGGGCAGGACCAGGATAAGCTCGGTTCGTG 195
Db   47 GlnAsnIleSerLeuAspGluLeuValIleValPheThrTrpGlnAspGlnAsnLeuVallLeu 66

Qy 196 TACGGAGCTATACAGAGGCCAAAGAGAACCCTCAAAATGTTCATCGGCAAGTATAAGGGCCGC 255
Db   67 TyrGluLeuPheArgGlyLysGluAsnProGlnAsnValIleHisLeuLeuTyrLysGlyArg 86

Qy 256 ACAAGCTTTGACAAAGACAAATTCGACCCTGAGACTCCATAATATTCAGATCAAAGGACAAG 315
Db   87 ThrSerPheAspLysAspAsnTrpThrLeuArgLeuHisAsnValGlnIleLysLysAspLys 106

Qy 316 GGCCTTGTACCAAAGTTTCGTTCATCATAAAAGGCCCAAAGGACTCGGTTCCCATGCCACCAG 375
Db 107 GlyThrHisTyrHisCysPheIleHisTyrLysGlyProLysGlyLeuValProLysProMetHisGln 126

Qy 376 ATGAAATTCTGACCTATCAGTGCCTTGCTAACTTCAGTCAACCTGAAAATAATGGTAACTTCTT 435
Db 127 MetSerAspLeuSerValLeuAlaAsnPheSerGlnProGluIleThrValThrSer 146

Qy 436 AATAGAACAGAAAATTCTGGCCATCATAAAATTGACCTGCTCATCATACAAGGTTACCCA 495
Db 147 AsnArgThrGluAsnSerGlyIleLeuAsnLeuThrCysSerSerThrIleGlyTyrPro 166

Qy 496 GAACCCAAGGAGGATGTATTTTTGGTAAAAACCGAGAATTCAAGTACTAAGGTAACTTCT 555
Db 167 GluProLysGluMetTyrPheGlnLeuAsnThrGluAsnSerThrThrLysTyrAspTyr 186

Qy 556 GTCATGAAGAAATCTCAAAATAATGTCACAGAACTTCTATCAGCTTGTCC 615
Db 187 ValMetLysLysSerGlnAsnAsnValThrGluLeuTyrAsnValSerIleSerSerLeuPro 206

Qy 616 TTCTCAGTCCCTGGAGCGACATGTGACACTTCCTGTGTCTCTGCAACTTGAGTCAATG 675
Db 207 PheSerValProGluAlaHisAsnValSerValPheCysSerAlaLeuLeuGluThrHisLeu 226

Qy 676 AAG---CTTCCCCTACCTTATAATAGATGCACTACGAAA---CCCACCCTGAT 729
          ::: |||:::
Db 227 GluMetLeuLeuSerLeuProPheAsnIleAspProLysSerAspLysLysAspProGlu 246

Qy 730 GGGAGACCACATCCTCTGGATTGCGGCGTCTCGGCCTTGTAATGTTGGTCATTTTGTGGGGATG 789
Db 247 GlyLeuHisSerPheLeuTrpIleAlaAlaIleAlaIleLeuValMetPheValPheCysGlyMet 266

Qy 790 GTGTTCTTCTTACACTAAGGAAGCAAGTGGAAAGAGAGGAAAAGTACCGGTACCCAT 849
Db 267 ValSerPheLysSerThrLeuArgGlyLysArgLysSerGlnProGlyHisGluCys 286

Qy 850 GAAACCAACAAGTGGAGAGAAAAGAGTGAGCGAGGAAAAGTACCGGTACCAT 909
Db 287 GluThrArgLeuArgLysGlySerLysGlnThrArgValProTyrHis 306

Qy 910 GAAAGGAAAGATCTGATGAAGAGCCCAGTGTGTTAACATTTCGAAGACAGCTTCAGGCGGAC 969
Db 307 ValProLeuArgSerAspGluAlaGlnCysValAsnIleLeuLeuLysThrAlaSerGlyAlaAsp 326

Qy 970 AACAGT 975
Db 327 LysAsn 328

RESULT 7

ID   Q9BDM4
AC   Q9BDM4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD86 protein precursor.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21383618; PubMed=11491535;
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules";
RL   Immunogenetics 53:315-328(2001).
PRELIMINARY;   PRT;   323 AA.

SIGNAL
SQ   SEQUENCE   323 AA; 37019 MW; D211E103DB1A7D7A CRC64;   POTENTIAL.

Qy   180 MetLysLysSerGlnAsnAsnIleThrGluLeuThrTyrAsnValSerIleArgValSerLeu 199

Qy   619 TCAGTGCCTTGAAGCAAGCAAATGTGGAGCATCTTCGTCCTGCAACTTGAATGAAG 678
Db   200 ProIleProProGluThrAsnValSerIleValCysValLeuGlnLeuGluProSerLys 219

Qy   679 ------CTTCCCTCCCTTACCTTATATAATATAGATGCACATACGAAACCC-----ACC 723
Db   220 ThrIleLeuPheSerLeuProCysAsnIleAspAla------LysProProValGlnPro 237

Qy   724 CCTGATGAGACAGCCACATCCTCTGGATTCGGCCGTTCCTTGTAATGTTGGTCATTTGTGT 783
Db   238 ProValProAspHisIleLeuTrpIleAlaAlaAlaLeuLeuValThrValValValCys 257

Qy   784 GGGGATGGTGGTTCTTCTTAACACTAAGGAAAAGAAGAAGAAGAAGAAGAGCCTTGGCCCTCTCAT 843
Db   258 GlyMetValSerPheValThrLeuArgLeuArgLysLysLysSerGlnProSerAsn 277

Qy   844 GAATGT--GAAACCAACAAAGTGGAGAGAAAAGTGAGCAGAGAACCAAGAGAAAGAGTA 900
Db   278 GluCysGlyGluThrIleLysMetAsnArgLysAlaSerGluGlnThrLysAsnArgAla 297

Qy   901 CGGTACCCATGAAACAGGGAAAAGATCTGATGAAGGCCAGTGT---GTTAACAGTTCGAAGACA 957
Db   298 GluValHis------GluArgSerAspAspAlaGlnCysAspAspValAsnIleLeuLysThr 315

Qy   958 GCTTCAGCGGACGACAACAGTACTACACAGTTT 987
Db   316 AlaSerAspAspAsnSerThrThrAspPhe 325

RESULT 8

ID   Q9BDB8
AC   Q9BDB8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD86 protein precursor.
PRELIMINARY;   PRT;   323 AA.

Qy   79 AACATAAGCCTGGATGAGTGAGTTGGTAGTGTGTTTTGGCAGGACCAGGATAAGCTGGTTCTGTAC 198
Db   21 LysIleGlnAlaTyrPheAsnGluThrAlaAspLeuProCysQlnPheAlaAsnSerGln 40

Qy   139 AAGAGTCAAGCATATTTCAACAACAGACTGAGAACTGCCATGCCCATTTTACAAATTCTCAA 138
Db   41 AsnArgSerLeuSerGluLeuValValPheTrpGlnAsnGlnAsnLeuValLeuAsn 60

Qy   199 GAGCTATACAGAGGCAGAAAGATGCAAAGACAAACCCTCAAAATGTTTCATCGACAGTATAAGGGCCGCACA 258
Db   61 GluValTyrLeuGlyLysGluLysPheAspSerValHisSerLysTyrMetGlyArgThr 80

Qy   259 AGCTTTGACAAAGACAAATTGGAACCCTGGAGCTCCATAATTCAGATCAAGGACAAAGGGC 318
Db   81 SerPheAspLysAspLysLeuTrpIleLeuArgLeuHisAsnLeuGlnIleLysAspLysGly 100

Qy   319 TTGTATCAATGTTTCGTTCATCATAAAAGGGCCCAAAAGGACTCGGTTCCCATGCATGAATG 378
Db   101 LeuTyrGlnCysIleIleHisHisLysLysProProThrGlyMetIleArgIleHisGlnMet 120

Qy   379 AATTCTGACCTATCAGTGCTTGCTAACTTCAGTGAACAAATAATGGTAACTTCTAAT 438
Db   121 AsnSerGluLeuSerValLeuAlaAsnPheSerGlnProGluIleValProIleSerAsn 140

Qy   439 AGAACAGAAAATTCTGGCATCATAAAATTTGACCTCTCATCCATACAAGGTTACCCAGAA 498
Db   141 IleThrGluAsnMet---TyrIleAsnLeuThrCysSerSerIleHisGlyTyrProGlu 159

Qy   499 CCCAAGGAGAATGTAFTTTTFTGGGTAAAAAAACCGAGAATTCAAGTACTAAGTATGAATACTGTG 558
Db   160 ProGluLysMetSerValLeuLeuArgThrLysAsnSerThrIleGluTyrAspGlyVal 179

Qy   559 ATGAAGAAATCTCAAAATAATGTCACAGAGAACTCTACAACGTTTCTATCAGTGTCCTTC 618
Db   180 MetGlnLysSerGlnAsnAsnValThrGluAsnSerThrThrPheLeuSerValSerVal 199

Qy   619 TCAGTGCCTGAA---GCAAGCAATGTGAGCACTCTTCGTGTCCTGCAACTTGAGTGAATG 675
Db   200 SerPheProAspValThrSerAsnMetThrIlePheCysValLeuGluThrAspLysThr 219

Qy   676 AAGCTTCCCCCCTCACCTTATATAATATAGATGCACATACGAAACCACCACCCTCGATGGAGAC 735
Db   220 GlnLeuLeuSerSerProPheSerIleGluLeuGlu---AspProGlnProProAsp 238

Qy   736 CACATCCTCTGGGATTGCGGCGTTCCTTGTAAGTGTGGTCATTTGTGTGGGGGATGGTGTTC 795
Db   239 HisIleProTrpIleThrAlaValLeu---ProThrValIleIleCysValMetAlaPhe 257

Qy   796 TTTCTTAACACTAAGGAAA---AGGAAGAAGAAGCAGCCTGGCCCCTCTCACTGAAATGTGAA 852
Db   258 CysLeuIleLeuLeuTrpLysTrpLysLysLysLysGlnProArgAsnSerTyrLysLysCysGly 277

Qy   853 ACCAAAACAAAGTGGAGAGAAAAAGAGTGAGCAGACCAAGAGAAAGAGTACGGTACCCATGAA 912
Db   278 ThrLysThrLysTrpGluArgGluLysSerGluGlnThrLysArgLysSerIleLeuAsnVal 297

Qy   913 ACGGAAAGATCTGATGAAGGCCCAGTGTGTTGTTAACATTTCG---AAGACAGCTTCAGCGCGAC 969
Db   298 ProGluArgSerAspAspGluAlaGlnCysValPheLysSerLeuLysThrProSerCysAsp 317

Qy   970 AACAGTACTACACAGTTT 987
Db   318 LysSerAspThrArgPhe 323

US-10-790-396-9 (1-987) x Q9BDM4 (1-323)

Alignment Scores:
Pred. No.:
Score: 7.47e-86
Percent Similarity: 76.38%
Best Local Similarity: 61.96%
Query Match: 56.10%
DB: 6

                              Length: 323
                              Matches: 202
                              Conservative: 47
                              Mismatches: 71
                              Indels: 6
                              Gaps: 6

Qy   19 ATGGAAACTGAATAACAATTCTCTTTGATGAGACCCCCGCTATGGTGGTGCTTCCCATG 78
Db   1 MetGlyLeuSerAsnIleLeuPheValMetAlaPheLeuLeuSerGlyAlaAlaProLeu 20

RESULT 6

ID   002838   PRELIMINARY;   PRT;   325 AA.
AC   002838;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   B7-2.
GN   CD86.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97047772; PubMed=8892613;
RA   Maher S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,
RA   Bothwell A.L.;
RT   "Porcine endothelial CD86 is a major costimulator of xenogeneic human
RT   T cells: cloning, sequencing, and functional expression in human
RT   endothelial cells.";
RL   J. Immunol. 157:3838-3844(1996).
DR   EMBL; L76099; AAB61307.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM004406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   325 AA; 36527 MW; 988BE08137B0597D CRC64;

Alignment Scores:
Pred. No.:   1.01e-82
Score: 996.50
Percent Similarity: 70.12%
Best Local Similarity: 61.59%
Query Match: 67.47%
DB: 6

US-10-790-396-19 (1-840) x 002838 (1-325)

Length: 325
Matches: 202
Conservative: 28
Mismatches: 41
Indels: 57
Gaps: 5

Qy   19 ATGGAACTGAATAACATTCTCTTGTGGATGACCCTCCTGCTCTTCATG   78
Db   1 MetGlyLeuSerAsnIleLeuPheValMetValLeuLeuLeuSerGlyAlaAlaSerLeu   20

Db   21 LysSerGlnAlaThrTyrPheAsnGluThrTyrGlyLeuProCysHisPheThrAsnSerGln   40

Db   41 SerPheAspGlnAlaThrTrpThrLeuArgLeuHisAsnValGlnIleLysLysAspSerGly 100

RESULT 7

Q9BDN9

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ID   Q9BDN9      PRELIMINARY;      PRT;   275 AA.
AC   Q9BDN9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD86 protein precursor.
OS   Papio anubis (Olive baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Papio.
OX   NCBI_TaxID=9555;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21383618; PubMed=11491535;
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
DR   EMBL; AF344836; AAK37532.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig-v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Signal.
FT   SIGNAL        1     17       POTENTIAL.
SQ   SEQUENCE   275 AA;  31343 MW;  3AAD3481B4F37C19 CRC64;
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Alignment Scores:
Pred. No.:

Score:	881.50
Percent Similarity:	78.99%
Best Local Similarity:	63.77%
Query Match:	59.68%

Length:	275
Matches:	176
Conservative:	42
Mismatches:	55
Indels:	3
Gaps:	3

3.42e-72

US-10-790-396-19 (1-840) x Q9BDN9 (1-275)

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Qy  240 ProAspHisIleLeuTrpIleAlaAlaLeuLeuValThrValValValValCysGlyMet 259
                                                                       
Db  702 ............................................................ 702

Qy  260 ValSerPheValThrLeuArgLysGlyLysGlyGlnProGlySerAsnGluCys 279

Db  703 ---GAAACCAACAAAGTGGAGAGAGGAAAAGAAAAAGTGAGCGAAGGCAAGAGAGTACGGGTAC 759

Qy  280 GlyGluThrIleLysMetAsnArgLysAlaSerGluGlnThrLysAspArgGluVal 299

Db  760 CATGAAACGGAAAGATCTGATGAAGCCCAGTGT---GTTAACATTTGAAGACAGCTTCA 816

Qy  300 His------GluArgSerAspAspAlaGlnCysAspValAsnIleLeuLeuLysThrAlaSer 317

Db  817 GGCGACAAACAGTACACACAGTGTT 840

Qy  318 AspAspAsnSerThrThrAspPhe 325
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RESULT 8

Q9BDM4

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ID   Q9BDM4      PRELIMINARY;      PRT;   323 AA.
AC   Q9BDM4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD86 protein precursor.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21383618; PubMed=11491535;
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
DR   EMBL; AF344857; AAK37540.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig-v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Signal.
FT   SIGNAL        1     17       POTENTIAL.
SQ   SEQUENCE   323 AA;  37019 MW;  D21IB1O3DB1A7D7A CRC64;
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Alignment Scores:
Pred. No.:

1.55e-70   Length: 323

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Qy  259 AGCTTTGACAAGACAATTGGACCCTGAGACTCCATAATATTCAGATGAAGGACGAAAGGGC 318
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Db   81 SerPheAspProGluSerTrpThrLeuArgLeuHisAsnLeuGlnIleLysAspGluGly 100

Qy  319 TTGTATCAAGTTTCGTTCATCTGAATTCAGGAGGCCCAAAGGAACTCGTTCCATGCACCAGATG 378
Db  101 LeuTyrGlnCysIleLeuHisHisLysArgProThrGlyMetIleArgIleHisGlnMet 120

Qy  379 AATTCTGACCTATCAGTGCTTGCCTTAACTTCAGTCAACCTGACTGAAAAATAATGTTAACTTCTAAT 438
Db  121 AsnSerGluLeuSerValLeuAlaLeuThrSerValAsnLeuThrGluLys 140

Qy  439 AGAACAGAAAATTCTGGCATCATAAAATTTGACCTGCTCATCATACAACAAGGTTACCCAGAA 498
Db  141 IleThrGluAsnMet---TyrIleAsnLeuThrCysSerSerSerIleHisGlyTyrProGlu 159

Qy  499 CCCAAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGACTAAGTACTAATGTATGTC 558
Db  160 ProLysGluMetSerValLeuLeuArgThrLysAsnSerThrIleGluThrArgProGlyVal 179

Qy  559 ATGAAGAAATCTCAAAATAATGTCACAGAACTCAACAGTTCTATCAGCTGGTGCCCTTC 618
Db  180 MetGlyLysSerGlnAspAsnValThrGluLeuThrTyrAspValSerIleSerGlnValSerVal 199

Qy  619 TCAGTCCCTGAA---GCAAGCAAATGTGAGCAATCTTCGTGTCCTGCCACTTGACTGTCAATG 675
Db  200 SerPheProAspValThrSerAsnMetThrIlePheCysValLeuGluGlnThrArgLysThr 219

Qy  676 AAGCTTCCCTCCTTACTTATATATATAGAAAACCAACAAAGTGGAGAGAAAGAAAAAGTGAG 735
Db  220 GlnLeuLeuSerSerProPheSerIleGlyThrAsnThrMetGluArgGluGluSerGlu 239

Qy  736 CAGACCAAGAAAAGAGTACGGGTACCATGAAACGGAAAGATCTGATGAAGCCCAGTGTGTT 795
Db  240 GlnThrLysLysArgGlyLysIleAsnValProGluArgSerAspAspAlaGlnCysVal 259

Qy  796 AACATTTCG---AAGACAGCTTCAGGCGACAACAGTACTACACAGTTT 840
Db  260 PheLysSerLeuLysThrProSerCysAspLysSerAspThrIlePhe 275
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US-10-790-396-19 (1-840) x Q9BDM4 (1-275)

Qy   19 ATGGAACTGAATAACATTCTCTTTGTGATGACCCTCCCTGCTCTTATGGTGTGCTTCCATG 78
Db    1 MetGlyLeuSerAsnIleLeuPheValMetAlaPheLeuLeuSerGlyAlaAlaProLeu 20

Qy   79 AAGAGTCAAGACATATTTCAACAAGACTGGCAGAACTGCCATTTACAAAATTCTCAA 138
Db   21 LysIleGlnAlaTyrPheAsnGluThrAlaAspLeuProCysGlnPheAlaAsnSerGln 40

Qy  139 AACATAAGGCCTCGGATGAGTTGGTAGTGTTTGGCAGATAAGCTGGTTCTGTAC 198
Db   41 AsnArgSerLeuSerGluLeuValValPheTrpGlnAspGluAsnLeuValLeuAsn 60

Qy  199 GAGCTATACAGAGGCAAAAGAGACCTCAAAATGTTCATCGCAGTATAAGGGCCGCACA 258
Db   61 GluValTyrLeuGlyLysGluGluLysTyrMetGlyArgThr 80
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Alignment Scores:
Pred. No.:

Left panel

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                    SQNISLSDLVVFWQDDKLVLYELYRGKENPDNVHRYKYGRTSFDSKDNWTLRLHNIOI
                    KDKGLYQCFVHHKGPKGLVPMIQMNSDLSVLANFSQPEIMTSNRIENSGIINLTCSS
                    IQGYPEPKEMYFLVKTENSSTKYDTVMKKSQNNVTELYNVSLSLSFSVPEASNVSIFC
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                    TTQF"

       3'UTR        850..1795
                    /gene="CD86"
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ORIGIN
Query Match   71.3%; Score 704; DB 4; Length 1795;
Best Local Similarity 99.3%; Pred. No. 2e-178;
Matches 707; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy    1 ATGTATCTCAGATGCACTATGGAACTGAATAACATTCTCTTTGTGATGACCCTGCTC   60
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Db    7 ATGTATCTCAGATGCACTATGGAACTGAATAACATTCTCTTTGTGATGACCCTGCTC   66

Qy   61 TATGGTGCTGCTTCCATGAAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGC  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   67 TATGGTGCTGCTTCCATGAAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGC  126

Qy  121 CATTTTACAAATTCTCAAAACATAAGCCTGGATGATCAGTTGGTAGTGTTTTGGCAGGACCAG  180
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Db  127 CATTTTACAAATTCTCAAAACATAAGCCTGGATGATCAGTTGGTAGTGTTTTGGCAGGACCAG  186

Qy  181 GATAAGCTGGTTCTGTACGAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGC  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  187 GATAAGCTGGTTCTGTACGAGCTATACAGAGGCAAAGAGAACCCTCAAAATGTTCATCGC  246

Qy  241 AAGTATAAGGGCCGCACAAGCTTTGACAAAGACATTGGACCCTGAGACTCCATAATATT  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  247 AAGTATAAGGGCCGCACAAGCTTTGACAAAGACATTGGACCCTGAGACTCCATAATATT  306

Qy  301 CAGATCAAGGACAAGGGCTTGTATCAAATGTTTCATCATAAAGGGCCCAAAGGACTC  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  307 CAGATCAAGGACAAGGGCTTGTATCAAATGTTTCATCATAAAGGGCCCAAAGGACTC  366

Qy  361 GTTCCCATCCACCAGATGAATTCTGACCTATCCAGTCTCAGTCTCAAACCTGAA  420
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Db  367 GTTCCCATCCACCAGATGAATTCTGACCTATCACTGCTTGCTAACTTCAGTCTCAAACCTGAA  426

Qy  421 ATAATGGTAACTTCTAATAGAACAGAAAATTCTGGCCATCATAAAATTGACCTGCTCATCC  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  427 ATAATGGTAACTTCTAATAGAACAGAAAATTCTGGCCATCATAAAATTGACCTGCTCATCC  486

Qy  481 ATACAAGGTTACCCAGAACCCAGAGAGTGTATTTTTGGTAAAAACCAGAATTCAAGT  540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  487 ATACAAGGTTACCCAGAACCCAGAGAGTGTATTTTTGGTAAAAACCAGAATTCAAGT  546

Qy  541 ACTAAGTATGATACTGTCATGAAGAAATCTCAAAATAATCTCAAACGGTT  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  547 ACTAAGTATGATACTGTCATGAAGAAATCTCAAAATAATCTCAAACGGTT  606

Qy  601 TCTATCAGCTTGTCCTTCTCAGTCCCTGAAGCAAGCAAATGTGAGCAATCTTCTGTGTCCTG  660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  607 TCTATCAGCTTGTCCTTCTCAGTCCCTGAAGCAAGCAAATGTGAGCAATCTTCTGTGTCCTG  666

Qy  661 CAACTTGAGTCAATGAAGCTTCCCCTCCTCCCTACCTTATTATAATATAGAAACCAACA  712
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  667 CAACTTGAGTCAATGAAGCTTCCCCTCCTCCCTACCTTATTATAATATAGAAACCAACA  718
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Right panel

FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
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                     /cell_type="endothelial"
                     /clone_lib="3"
                     /dev_stage="adult"
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                     /gene="CD86"
     CDS   1..978
                     /gene="CD86"
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                     /note="putative"
                     /codon_start=1
                     /protein_id="AAB61107.1"
                     /db_xref="GI:2198559"
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                     QCFIHHKGPHLVPIHQMSSDLSLLANFSQPEINLLTNRTENSVINLTCSSTQGYPEP
                     QRMYMLINTKNSTTEHDADMKKSQNNITELYNVSIRVSLPIPETNVSIVCVLQEPS
                     KTLLFSLPCNIDAKPPVQPVPDHLIWIAALLVTVVVCCGMVSFVTLRKKKQPGPS
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     3'UTR   979..994
                     /gene="CD86"
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                     /gene="CD86"
                     /evidence=experimental

ORIGIN
Query Match   62.8%; Score 620; DB 4; Length 994;
Best Local Similarity 81.3%; Pred. No. 8.7e-156;
Matches 800; Conservative 0; Mismatches 160; Indels 24; Gaps 6;

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Qy   19 ATGGAACTGAATAACATTCTCTTTGTTGATGACCTCCTTGCTCTATGGTGTGCTTCCATG   78
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGGAACTGAATAACATTCTCTTTGTTGATGACCTCCTTGCTCTATGGTGTGCTTCCTTG   60

Qy   79 AAGAGTCAAGCATATTTCAACAAGACTGGAGAACTGCCATGCCATTTACAAATTCTCAA  138
        ||| |||||| |||||||||||  ||||||||||||||||  | ||||||||  | | |
Db   61 AAAAGTCAGGCATATTTCAATGAGACTGGAGAACTGCCGTTGCCATTTACAAAACTCGGCAG  120

Qy  139 AACATAAGCCTGGATGATCAGTTGGTAGTGTTTTGGCAGGACCAG  198
        |||| |||||||||||||| || || | ||||||||||||||||
Db  121 AACCTAAGCCTGGATGAGCTGGTCATATTTTGGCAGGACCAGGATAACATTGTTCTAC  180

Qy  199 AACACAAGCCTGGACAAAGGACAAGAACCCTCAAAAATGTTCATCGGCGGAAGTAAGACTGGGCA  258
        |||  |||||||||    ||     ||||| |||||  |||| |||| |||||  ||| ||||
Db  181 GAGCTATACCGAGGCCAAGAGAAGCCTCATAATGTTAATTCAAAGTATATGGGACGTACA  240

Qy  259 AGCTTTGACAAAGACAATTGGACCCTGAGACTCCACCTGAGACTCCACAACGTTCAAGGACAAGGGCA  318
        |||||||||||| ||     ||||||| ||||||| || |||||| | | |||||||||| ||||
Db  241 AGCTTTGACCAGGCCACCTGGACCCTGAGACTCCACAACGTTCAAATCAAGGACAAGGGC  300
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RESULT 9
BD237353

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LOCUS       BD237353                 994 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Improvement in tolerance to xenografts.
ACCESSION   BD237353
VERSION     BD237353.1  GI:33047123
KEYWORDS    JP 2002532115-A/6.
SOURCE      Sus sp.
  ORGANISM  Sus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 994)
  AUTHORS   Lechler,R.I., Rogers,N.J. and Dorling,A.
  TITLE     Improvement in tolerance to xenografts
  JOURNAL   Patent: JP 2002532115-A 6 02-OCT-2002;
            ML LABORATORIES PLC
COMMENT     Sus sp. (pig)
            PN   JP 2002532115-A/6
            PD   02-OCT-2002
            PF   17-DEC-1999 JP 200589212
            PR   19-DEC-1998 GB   9827921.9 23-OCT-1999 GB   9925015.1 PI
            ROBERT IAN LECHLER,NICHOLA JANE ROGERS,ANTHONY DORLING PC
            C12N15/09,A61K39/00,A61P37/06,C07K16/28,C12P21/08,C12N15/00 CC
            Improvement in tolerance to xenografts
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                     /organism="Sus sp."
                     /mol_type="genomic DNA"
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FH   Key             Location/Qualifiers
FT   source          1..994

ORIGIN
Query Match   62.8%;   Score 620;   DB 6;   Length 994;
Best Local Similarity   81.3%;   Pred. No. 8.7e-156;
Matches 800;   Conservative   0;   Mismatches 160;   Indels  24;   Gaps   6;
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Alignment (left):

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Qy  319 TTGTATCAATAGTTTCGTTCATCATAAAGGGGCCCAAAGGACTCGTTCCATCACCAGATG 378
Db  301 TCATATCAATGTTTCATCCATCATAAAGGGGCGCGCATGGGCATTGGTTCCTATCCAGATG 360

Qy  379 AATTCTGACCTATCAGTGCTTGCTAACTTCAGTGTTAACTTCTAAT 438
Db  361 AGTTCTGACCTATCATTGCTTGCTAACTTCAGTCAACCTGAAAT 420

Qy  439 AGAACAGAAAAATTCTGGCATCATAAAATTTGACCTGCTCATCTCATCCATACAGGTTACCCAGAA 498
Db  421 CACACAGAAAATTCTG---TCATAAATTTGACCTGCTCATCTACACAAGCTACCCAGAA 477

Qy  499 CCCAAGGAGGATGTATTTTTTGGTAAAAACCGAGAATTCAAGTACTACAAGTATGATACTGTC 558
Db  478 CCCCAGAGGATGTATATGTTTGCTAAAATACGAAGAATTCAACCACTGAGCATGATGATGACTGAC 537

Qy  559 ATGAAGAAATCTCAAAATAAATGTCACAGAACTCTACAACGTTCTATCAGCTTGTCCTTC 618
Db  538 ATGAAGAAATCTCAAAATAACATCACGGAACTCTACAATCTATCATCAGGGTGTCTCTT 597

Qy  619 TCAGTCCCTGAGGCAAGCAAATGTGAGCATCTTCTCGTGTGTCCCTGCAACTTGAGTCAATGAA- 677
Db  598 CCCATCCCTCCCGAGACAAAATGTGAGCACGTCGTGTCCCTGCAACTTGAGTCAATGAAGAAG 657

Qy  678 -----GCTTCCCTCCCTACCTTATAAATATAGATGCA--- 729
Db  658 ACACTGCTTTCTCCCTACCTTGTAATATAGATGCAAAGCCACTGTTCGCAACCCCCTGTC 717

Qy  730 GGAGACCACAATCCTCTGGAATGCGGCCTCGCTCCTGTAAATGTTGGTCATTTTGTTGTGGGATG 789
Db  718 CCAGACCACATCCTCTGGAATTGCAGCTCACTTGTAACAGTGGTCGTCGTTGTGTGGGATG 777

Qy  790 GTGTTCTTTCTAACACTAAGGAAAAGGAAGAAGGAAGCAGCCTGGCCCCTCCTCTCATGAAT-- 847
Db  778 GTGTCCTTTGTAACACTAAGGAAAAGGAAGAAGAGCAGCCTGGCCCCTCCTCTAATGAAATGT 837

Qy  848 -GTGAAACCAACAAAGTGGAGAGAGAAAAGTGAGCAGAGAAAAGAGTACGGTAC 906
Db  838 GGTGAAACCATCAAAATGAACAGAAGTGAGAAAGAGAAGAGCAGCCTG...GGTAC 897

Qy  907 CATGAAAACGGAAAGAATCTGATGAAGCCCAGTG---TGTTAACATTTCGAAGACAGCTTCA 963
Db  898 CAT------GAACGAATCTGATGAGTCCCAGTGTTGAATGTTAATATTTTAAAGACACCTCA 951

Qy  964 GGGGACAACAGTACTACACAGTTT 987
Db  952 GATGACAACAGTACTACACAGATTTT 975
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Alignment (right, Db 6):

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Qy   19 ATGGAAACTGAATAACATTCTCTTTGTGATGAACCCTCCTCCTATAGGTGCTGCTTCCATG 78
Db    1 ATGGGACTGAGTAACATTCCTTTGTGATGGTCTCCTCCTTGGCTCTCCTGGTGCTGCTTTG 60

Qy   79 AAGAGTCAAGCACATATTTCAACAAGACTGGAGAACTGCCATGCCATTTTACAAAATTCAA 138
Db   61 AAAAGTCAGGCATATTTTCAATGAGACTGGAGAACTGCCGTGCCATTTTACAAAACTCGGCAG 120

Qy  139 AACATAAGCCTGGATGAGTTGGTAGTGTTTGGGGGCAGGACCAAGAATAAGCTGGTTCTGTTAC 198
Db  121 AACCTAAGCCTGGATGAGGCTGGTCATATTTTTGGGCAGGACCAAGAATAACCTGGTTCTCTAC 180

Qy  199 GAGCTATACAGGGCGAAAAGACAACCCTCAAAAATGTTCATCGCAAGTAATAAAGGGCCGCCACA 258
Db  181 GAGCTATACCGAGGCCAAGAAGACCCTCATTAAATGTTAATTCCAAGTATATGGGTCGACA 240

Qy  259 AGCTTTGACAAAGACAATGGGAACCCTGGAGACTCCATAATATTCAGATCAAGGACAAGGGC 318
Db  241 AGCTTTGACCAGGCCACCTGGAGACCCCTGAGACTCCACAGTTCAAAATCAAGGACAAGGGC 300

Qy  319 TTGTATCAATAGTTTCGTTCATCATAAAGGGGCCCAAAGGACTCGTTCCATCACCAGATG 378
Db  301 TCATATCAATGTTTCATCCATCATAAAGGGGCGCGCATGGGCATTGGTTCCTATCCAGATG 360

Qy  379 AATTCTGACCTATCAGTGCTTGCTAACTTCAGTGTTAACTTCTAAT 438
Db  361 AGTTCTGACCTATCATTGCTTGCTAACTTCAGTCAACCTGAAAT 420

Qy  439 AGAACAGAAAAATTCTGGCATCATAAAATTTGACCTGCTCATCTCATCCATACAGGTTACCCAGAA 498
Db  421 CACACAGAAAATTCTG---TCATAAATTTGACCTGCTCATCTACACAAGCTACCCAGAA 477

Qy  499 CCCAAGGAGGATGTATTTTTTGGTAAAAACCGAGAATTCAAGTACTACAAGTATGATACTGTC 558
Db  478 CCCCAGAGGATGTATATGTTTGCTAAAATACGAAGAATTCAACCACTGAGCATGATGATGACTGAC 537

Qy  559 ATGAAGAAATCTCAAAATAAATGTCACAGAACTCTACAACGTTCTATCAGCTTGTCCTTC 618
Db  538 ATGAAGAAATCTCAAAATAACATCACGGAACTCTACAATCTATCATCAGGGTGTCTCTT 597

Qy  619 TCAGTCCCTGAGGCAAGCAAATGTGAGCATCTTCTCGTGTGTCCCTGCAACTTGAGTCAATGAA- 677
Db  598 CCCATCCCTCCCGAGACAAAATGTGAGCACGTCGTGTCCCTGCAACTTGAGTCAATGAAGAAG 657

Qy  678 -----GCTTCCCTCCCTACCTTATAAATATAGATGCA--- 729
Db  658 ACACTGCTTTCTCCCTACCTTGTAATATAGATGCAAAGCCACTGTTCGCAACCCCCTGTC 717

Qy  730 GGAGACCACAATCCTCTGGAATGCGGCCTCGCTCCTGTAAATGTTGGTCATTTTGTTGTGGGATG 789
Db  718 CCAGACCACATCCTCTGGAATTGCAGCTCACTTGTAACAGTGGTCGTCGTTGTGTGGGATG 777

Qy  790 GTGTTCTTTCTAACACTAAGGAAAAGGAAGAAGGAAGCAGCCTGGCCCCTCCTCTCATGAAT-- 847
Db  778 GTGTCCTTTGTAACACTAAGGAAAAGGAAGAAGAGCAGCCTGGCCCCTCCTCTAATGAAATGT 837

Qy  848 -GTGAAACCAACAAAGTGGAGAGAGAAAAGTGAGCAGAGAAAAGAGTACGGTAC 906
Db  838 GGTGAAACCATCAAAATGAACAGAAGTGAGAAAGAGAAGAGCAGCCTG...GGTAC 897
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                    /note="144 nucleotide insertion in Homo sapiens CD86"
ORIGIN

Query Match    62.0%;  Score 520.4;  DB 9;  Length 901;
Best Local Similarity 79.0%;  Pred. No. 1.8e-127;
Matches 659;  Conservative  0;  Mismatches 166;  Indels  9;  Gaps  3;

Qy    13 TGCACTATGGAAACTGAATAACACATTCTTCTTTGTTGTGATGGTTGGTCGTGCTGCT 72
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Db     1 TGCACTATGGAACTGAGTAACTGAGTAACATTCTTCTTTGTTGTGATGGTCGTGCTGCT 60

Qy    73 TCCAATGAAGAGTCAAGCATATTTCAACACAGACTGGAGACTGGCCATTGCCATTTTACCAAAT 132
         ||||||  || |||||||| |||||||||||||||||||||||||||||||||||||| ||||||
Db    61 CCCCTGAAGAAGTCAAGCATTATTTCAATGAGACTGCAGAAGCTTTGCCAAAATTTACAAAT 120

Qy   133 TCTCAAAACATAAGCCTCGAATGAGTGGTTGGTGAGTGTTGGTGGAGGACCCAGAGTAAGCTGGTT 192
         ||||||| ||  |||||||||||||||| ||||| |||||||||||||||||||||||||||||||
Db   121 TCTCAAAACCGAAGCCTGAGTGAGTGCTAGTGAGTATTTTTGGCAAGTAAGAGAAAACTTGGTT 180

Qy   193 CTGTACGAGCTATACAGAGGCAAAGAGAACCCTCAAAAATGTTCATGGCAAGTATATAAGGGGC 252
         |||||| |||||||||||||||||||| | |||||||| |||| |||||||| |||||| |||||
Db   181 CTGAATGAGGTATACTTAGGCGCAGAGGAGAAAAATTTGACAGCGTTCATTCCAAGTAATGGGGC 240

Qy   253 CGCACAAGCTTTGACAAAGACAAATTGGACCCCTGAGACTCACATAATATTCAGATCAAGGAC 312
         ||||||| |||||||||||| |||||||| ||||||||| ||||| |||||| |||| |||||
Db   241 CGCACAAGTTTTGATCCGGAGAGTTGGACCCTCGAGCCTTCACAACCTTCAGATCAAGGAC 300

Qy   313 AAGGGCTTGTATCAATGTTTCGTTCATCATAAAAGGGCCCCAAAAGGACTCGTTCCCATGCAC 372
         |||||||||||||||||||||  |||||| |||||||||| ||| ||||| ||||| |||||
Db   301 AAGGGCTTGTATCAAGTGTATCATCATCCACAAAAAGGCCCACAAGGGATGATCCGCATCAC 360

Qy   373 CAGATGAAATTCTGACCTATCAGTGTCCTGCTAACCTCAGTGAAATAATGGGTAACT 432
         ||||| |||||||||  ||||||||| |||||| |||||||||| ||| ||| ||||
Db   361 CAGATGAATTCTGAACTGTCAGTGCTTGCTAGCTTCAGTGAAATAGTCCCAATT 420

Qy   433 TCTAATAGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCCATACAAGGTTAC 492
         |||||| ||||||||||||| |||||||||| |||||| ||| |||||| ||||||||||
Db   421 TCTAATATAACAGAAAA---TATGTACATAAATTTGACCTGCTCATCTATACACGGTTAC 477

Qy   493 CCAGAACCCAAAGAGAGATGTATTTTTTTGGTAAAAAACCGAGAATTCAAGTGTTCTAACAGCTTG 552
         |||||| || ||||| ||||| ||||||||||||||||| |||||||| |||||||| |||||||
Db   478 CCAGAACCTGAGAGAGAGTCGTTTGCTAGAACCAAGAATTCAC|TATTCGAGTAATGAT 537

Qy   553 ACTGTCATGAAGAAATCTCAAAATAATAATGTCACAGAACTCTACAAACGTTTCTATCAGCTTG 612
         |||||||| |||||||  |||||| ||| || ||||||||| ||||| |||||||||||||||
Db   537 GGTGTTATGCAGAAATCTCAGATAATGTCACAGAACTGTACGAGACTTTCCATCAGCTTG 597

Qy   613 TCCTTCTTCAGTGCCTGAAG---CAAGCAATGTGAGCATCTTCTGTGTGTCCTGCAACTTGAG 669
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Db   598 TCCTGTTTCATTCCCTGATGTTACGAGCAACATGACCAATCTTCTGTGTTCTGGAAACTGAC 657

Qy   670 TCAATGAAAGCTTCCCTCCTCCCTACCTTATAAATTATGAGAAAATATGGGAAGGAAAAGAA 729
         ||||||||||||||||||||| ||  |||||| |||| ||||| |||| |||||||||||||
Db   658 AAGACACAGCTTTTATCCTCACCTTTCTCTATAGGAACCACAACAAAGAGGAGGGAAGAG 717

Qy   730 AGTGAGCAGCAAGAGGAAGAGTACGGGTACCATGAAGAGGAAAGATCTGAATGAAGCCCAG 789
         |||||| |||| |||||| |||| ||||| |||| |||| |||||| ||| |||||||||
Db   718 AGTGAGCAGACCAAAAAGAGAGAAAATTAATGTACCTGAAAGGATCTGATGAAGCCCAA 777

Qy   790 TGTG---TTAACATTTGCAAAGACACCTTCAGGCGGCAACAGTACTACACAGTTT 840
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Db   778 TGTGTTTTTAAAGTTTGAAGACACCTTCATGGGACAAAAGTGATACCATTTT 831
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RESULT 9

LOCUS       PIGCD86G         994 bp    mRNA    linear   MAM 17-JUN-1997
DEFINITION  Sus scrofa CD86 mRNA, complete cds.
ACCESSION   L76099
VERSION     L76099.1  GI:2198558
KEYWORDS    T cell costimulation.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 994)
  AUTHORS   Maher,S.E., Karmann,K., Min,W., Hughes,C.C., Pober,J.S. and
            Bothwell,A.L.
  TITLE     Porcine endothelial CD86 is a major costimulator of xenogeneic
            human T cells: cloning, sequencing, and functional expression in
            human endothelial cells
  JOURNAL   J. Immunol. 157 (9), 3838-3844 (1996)
  MEDLINE   97047772
   PUBMED   8892613
COMMENT     GSDB:S:74002
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9823"
                     /cell_line="PEC-A"
                     /cell_type="endothelial"
                     /clone_lib="3"
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                     /gene="CD86"
                     /standard_name="B7-2"
                     /note="putative"
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                     /protein_id="AAB61307.1"
                     /db_xref="GI:2198559"
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                     QCFIHRGPHGLVPIHQMSDLSLLANFSQPEINLLTNHTENSVINILTCSSTQGYPEP
                     QRVMLLNTKNSTEEHDAMKKSQNNITELIYNVSIRVSLPIPPETNVSIVCVLQLEPS
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                     /gene="CD86"
                     /note="putative"
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ORIGIN

Query Match    57.6%;  Score 484;  DB 4;  Length 994;
Best Local Similarity 83.0%;  Pred. No. 8.5e-118;
Matches 579;  Conservative  0;  Mismatches 110;  Indels  9;  Gaps  2;

Qy    19 ATGGAACTGAATAACATCTTCTTTGTTGTGATGACCCTCCTGCTTCCTATGGTTGCTGCTTCCATG 78
         |||||||||||||||  ||||||||||||||| ||||| |||||||||||||||| ||||||||
Db     1 ATGGGACTGAGTAACATTCTCTTTGTGATGGTTCTCCTGCTCTCGGGTAATGCTTCC 60

Qy    79 AAGAGTCAAGCATATTTCAACAAGACTCGAGAGAACTGCCCATGCCATTTTACAAAATCTCAA 138
         |||||||||| ||||||||||  ||||| |||||||| ||||| ||||||||||||||| |||
Db    61 AAAAGTCAGGCATATTTCAATGAGACTGGAGAACTGCCGTGCCATTTTACAAACTCTCAG 120

Qy   139 AACATAAGCCTGGATGAGTTGGTAGTGTTTTGGCAGGACCAGGATAAGCTGGTTCTGTAC 198
         ||||||||||| ||| |||||| |||||| ||||||||||||| ||| |||||| |||||
Db   121 AACCTAAGCCTGGATGAGCTGGTCATATTTTGGCAGGACCAGGATAACCTGGTTCTCTAC 180

Qy   199 GAGCTATACAGAGGACAAAGAGAACCCTGAGACTCACGCAACTTCAGGGGGCCACA 258
         |||||||||| ||| || ||||| ||||| || | ||| |||||| ||||||||||
Db   181 GAGCTATACCGAGGCCAAGAGAAGCCTCATAATGTTAATTCCAAGTATATGGGTCGGCCACA 240

Qy   259 AGCTTTGACAAAGACAAATTGGACCCCTGAGACTCCATAATATTCAGATCAAGGACAAGGGC 318
         ||||||||||| ||||||| || |||| ||| | |||  | |||||||||| |||||||||
Db   241 AGCTTTGACCAGGCCACCTGGGACTCCACAAATCAAGGACAAGGGC 300

Qy   319 TTGTATCAAGTGTTTCGTTCATCATCAAGGACTCCAGGAAGGGACAAGGGC 378
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TTGTATCAAGTGTTTCGTTCATCATCAAGGACTCCAGGAAGGGACAAGGGC 378
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RESULT 10

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LOCUS       BD237353    994 bp    DNA    linear    PAT 17-JUL-2003
DEFINITION  Improvement in tolerance to xenografts.
ACCESSION   BD237353
VERSION     BD237353.1  GI:33047123
KEYWORDS    JP 200253115-A/6.
SOURCE      Sus sp.
  ORGANISM  Sus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 994)
  AUTHORS   Lechler,R.I., Rogers,N.J. and Dorling,A.
  TITLE     Improvement in tolerance to xenografts.
  JOURNAL   Patent: JP 200253115-A 6 02-OCT-2002;
            ML LABORATORIES PLC
COMMENT     OS   Sus sp. (pig)
            PN   JP 200253115-A/6
            PD   02-OCT-2002
            PF   17-DEC-1999 JP 200589212
            PR   19-DEC-1998 GB 9827921.9,23-OCT-1999 GB  9925015.1 PI
            ROBERT IAN LECHLER NICHOLA JANE ROGERS,ANTHONY DORLING PC
            C12N15//09,A61K39/00,A61P37/06,C07K16/28,C12P21/08,C12N15/00 CC
            Improvement in tolerance to xenografts;
FEATURES             Location/Qualifiers
     source          1. .994
                     /organism="Sus sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9826"
ORIGIN
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Query Match             57.6%;  Score 484;  DB 6;  Length 994;
Best Local Similarity   83.0%;  Pred. No. 8.5e-118;
Matches  579;  Conservative  0;  Mismatches 110;  Indels  9;  Gaps  2;

Qy     19  ATGGAACTGAATAAACATTCTCTTTGTGATGACCCTGTCGTGCTGCTTCCATG  78
           ||||  |||||| || |||||| |||||||| |||| ||| || || || |
Db      1  ATGGGACTGAGTAACATTCTCTTTGTGATGGTCCTGTCCGTGCTGCTTCCTG  60

Qy     79  AAGAGTCAAGCATATTCAACAAGACTGGAGAACTGCCGTGCCATTTTACAAAATCTCCAA  138
           |||| ||||||| || ||  || || ||||||||  |  | || ||| ||| |||| |
Db     61  AAAAGTCAGGCATATTCAATGAGACTGGAGAACTGCCGTGCCATTTTTACAAAATCTGGCAG  120

Db    301  TCATATCAATGTTCATCCATCATAAAGGGCCGCATGGACTTGTTCCTATCCACCAGATG  360
Qy    379  AATTCTGACCTATCAGTGCTTGCTTGCTCAGTCAAC...TTAAT  438
Db    361  AGTTCTGACCTATCAGTGCTTGCTTGCTCAGTCAAC...TAAT  420
Qy    439  AGAACAGAAAAATTCTGGCATCATAAATTGACCTGCTGCTCA...CCAGAA  498
Db    421  CACACAGAAAAATTCTG---TCATAAATTGACCTGCTCATCTCA...CAGA  477
Qy    499  CCCAGGAGATGTATTTTTGGTAAAAACCGAGAATTCAAGTACTAAGTATACACTGTC  558
Db    478  CCCCAGAGGACGTATATGTTGGCTAAATACGGAAGAATTCAACCA...GATGTGAC  537
Qy    559  ATGAAGAAATCTCAAAAATAAGTCACAGAACTTC...TGCTTC  618
Db    538  ATGAAGAAATCTCAAAATAACATCACGGAACTTCTA...TCTT  597
Qy    619  TCAGTCCCTGAAGCAGCAAGCAATGTGAGCGA...CAATGAA-  677
Db    598  CCCATGCCTCCGAGACAAAGTGAGCATCGTCTC...CAGCCAAGCAAG  657
Qy    678  -----GCTTCCCTCCCTACCTTATAATATATAGAAACCAA  710
Db    658  ACACTGCTTTTCTCCCTACCTTGTAATATAGATGCAA  695
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RESULT 11

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LOCUS       AX027016    994 bp    DNA    linear    PAT 16-SEP-2000
DEFINITION  Sequence 13 from Patent WO0037102.
ACCESSION   AX027016
VERSION     AX027016.1  GI:10188045
KEYWORDS    .
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1
  AUTHORS   Rogers,N.J., Dorling,A. and Lechler,R.I.
  TITLE     Immunosuppression
  JOURNAL   Patent: WO 0037102-A 13 29-JUN-2000;
            ROGERS NICHOLA JANE (GB) ; DORLING ANTHONY (GB) ; ML LAB PLC (GB) ;
            LECHLER ROBERT IAN (GB)
FEATURES             Location/Qualifiers
     source          1. .994
                     /organism="Sus scrofa"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9823"
ORIGIN
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Query Match             57.6%;  Score 484;  DB 6;  Length 994;
Best Local Similarity   83.0%;  Pred. No. 8.5e-118;
Matches  579;  Conservative  0;  Mismatches 110;  Indels  9;  Gaps  2;

Qy     19  ATGGAACTGAATAAACATTCTCTTTGTGATGACCCTGTCGTGCTGCTTCCATG  78
           ||||  |||||| || |||||| |||||||| |||| ||| || || || |
Db      1  ATGGGACTGAGTAACATTCTCTTTGTGATGGTCCTCTCGGCGTCCTCCTTTG  60

Qy    139  AACATAAGCCTGGAGTGGAGTTGGTAGTGGTGTTTGGCAGGACCAGGAGGATAAGCTGGTTCTGTAC  198
Db    121  AACCTAAGCCTGGAGTGAGCTGGTCATATATTTGGCAGGACCAGGAGGATAACCTGGTTCTCTAC  180
Qy    199  GAGCTATACAGAGGCAAAGAGAGAAACCCTCAAAATGTTCATCGCAAGTAGTAAAGGCCGCACA  258
Db    181  GAGCTATACCGGAGGCCAAGAGAGAAAGCCTCATAAAGTTGAATTCCAAGTAATATGTCGCACA  240
Qy    259  AGCTTTGACAAAGACAAATTGACCCCTGTAGACTCCATAATATTCAGATCAAGAGGACAAGGGC  318
Db    241  AGCTTTGACCAGGCCACCTGGACCCTGACCTCACAACGTTCAAATCAAGAAGGACAAGGGC  300
Qy    319  TTGTATCAAGTTTTCGTTCATCATCATAAAGGGCGGCCCAAAGGACTCGTTCCCAAGGCACCAGAT  378
Db    301  TCATATCAATGTTCATCCATCATAAAGGGCGGCCCAAAGGACTCGTTCCCATGCAAGGCACCAGATG  360
Qy    379  AATTCTGACCTATCAGTGCTTGCTGCTCAGTCAACATAATATGGTAAATGAATTTTTAAT  438
Db    361  AGTTCTGACCTATCAGTGCTTGCTGCTCAGTCAACATAATATGGTAAATGAATTTTAAT  420
Qy    439  AGAACAGAAAAATTCTGCCATCATAAAATTTGACCTGCTGCTCATCTCATCCATAAGGTTACCAGAA  498
Db    421  CACACAGAAAAATTCTG---TCATAAATTGACCTGCTCATCTCATCCATAAGGTTACCAGAA  477
Qy    499  CCCAGGAGATGTATTTTTTGGTAAAAACCGAGAATTCAAGTACTAAGTATGATACTGTC  558
Db    478  CCCCAGAGGACGTATATGTTGGCTAAATACGGAAGAATTCAACCACTGAGCAATGATGTGAC  537
Qy    559  ATGAAGAAATCCAAAAATAAGTCACAGAACGTTCTATCAGCTTGTCCTTC  618
Db    538  ATGAAGAAATCTCAAAATAACATCACGGAACTTCTACAAATGATCAATCAGGGGTGTCTCTT  597
Qy    619  TCAGTCCCTGAAGCAGCAAGCAATGTGAGCGATCTCTGTGTCCCTCGGAACAGTGAGTCAAATGAA-  677
Db    598  CCCATGCCTCCGAGACAAAGTGAGCATCGTCTCGTGTCCTGCAACTTGAGCCAAGCAAG  657
Qy    678  -----GCTTCCCTCCCTACCTTATAATATATAGAAACCAA  710
Db    658  ACACTGCTTTTCTCCCTACCTTGTAATATAGATGCAA  695
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RESULT 9
US-08-479-744A-1

Sequence 1, Application US/08479744A
Patent No. 6084067

GENERAL INFORMATION:
 APPLICANT: Freeman, Gordon J.
 APPLICANT: Nadler, Lee M.
 APPLICANT: Gray, Gary S.
 TITLE OF INVENTION: CTLA4/CD28 Ligands and
 TITLE OF INVENTION: Uses Therefor
 NUMBER OF SEQUENCES: 55
 CORRESPONDENCE ADDRESS:
  ADDRESSEE: LAHIVE & COCKFIELD, LLP
  STREET: 60 State Street
  CITY: Boston
  STATE: Massachusetts
  COUNTRY: USA
  ZIP: 02109
 COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/479,744A
  FILING DATE: June 7, 1995
  CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/280,757
  FILING DATE: 26-JUL-1994
  APPLICATION NUMBER: 08/109,393
  FILING DATE: 28-AUG-1993
  APPLICATION NUMBER: 08/101,624
  FILING DATE: 26-JULY-1993
  APPLICATION NUMBER: 08/147,773
  FILING DATE: 3-NOV-1993
 ATTORNEY/AGENT INFORMATION:
  NAME: Mandragouras, Amy E.
  REGISTRATION NUMBER: 36,207
  REFERENCE/DOCKET NUMBER: RPI-004CP3
 TELECOMMUNICATION INFORMATION:
  TELEPHONE: (617) 227-7400
  TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
  LENGTH: 1120 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
  NAME/KEY: CDS
  LOCATION: 107..1093
US-08-479-744A-1

Query Match 58.3%; Score 575.2; DB 3; Length 1120;
Best Local Similarity 77.8%; Pred. No. 6.3e-172;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

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Qy     1  ATGTATCTCAGATGCACTATGGAAGTGAATAACATTCTCTTTGTTGATGATGACCTGTC   60
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Db   107  ATGGATCCCCAGTGCACTATGGGACTGAGTAACATTCTCTTTGTTGATGGCCTGTGTC  166

Qy    61  TATGGTGGCTGCTTCCATGAAGAGTCAAGCATATTTCAACAAGACGGGAACTGCCATGC  120
          |||||| ||| |  ||| || | |   |   ||| ||  || || ||||||   || ||
Db   167  TCTGGTTCGTTGCTCCCTGAGAAGATTCAAGCTTAATTCAATGAGACTGCAGAACATGC  226

Qy   121  CATTTTACAAAATTCTCAAAACATAAGCCTGGAATGAGGTTGGGTAGTGTTTTGGGAGG  180
          ||| || || | |||||||| || |   ||| |  || ||||||| | || ||||||||
Db   227  CAAATTGCAAAACTCCTCAAAAACCAAAGCCTGAGTGAGCTAGTAGTATTTGGGAGGAG  286

Qy   181  GATAAGCTTGGTTCTTGTACGAGCTATACAGAGAGGCAAAGAACCCTCAAAATGTTCATCGC  240
          |||| ||| ||| | ||  ||||| || |||||||| |   ||  ||||| | ||||||||
Db   287  GAAAACTTGGTTCTTGAATGAGGTATTACTTAGGCCAAAGAAAATTGACAGTGTTCATTCC  346

Qy   241  AAGTATAAGGGCCGCACAAGCTTGACAAAGACAATTGGACCCTGAGACTTCAAGT  300
          || |||| ||||| |||| || || || |||| ||| ||  ||||| || |||||
Db   347  AAGTATAGGGGCCGCACAGTTTTGATTCGGACAGTTGGGACCCTGAGACTTCAATTCTT  406

Qy   301  CAGATCAAGGACAAGGGGCCTTGTATCAAGTTTCGTTCATCATAAAGGGGCCAAAGGACTC  360
          || || ||||| ||||| ||||| ||| ||||  || || || ||||| ||| ||| ||
Db   407  CAGATCAAGGACAAGGGGCTTGTTATCAAGTATCATCCATCACAAAAAGCCCAGGAAATG  466

Qy   361  GTTCCCATGCCACCAGATGGAATTCTGACCTATCATCAGTGCTTGCTTGCTTCAGTCAGTC  420
          |  || ||| |||||||| |||||||||||| ||||||| |||||||| | ||||| |  
Db   467  ATTCCGCATCCACCACAGATGAATTCTTGAACTGTCAGTGCTTGTAACTTCAGTCAACCTGAA  526

Qy   421  ATAATGGTAACTTCTAATAGAACAGAAAATTCTGGGCATCATAAATTTGACCTGCTCATCC  480
          ||   ||||||||  | || |||| || | |||| | || || ||||||||| |  | ||
Db   527  ATAGTACCAAATTTCTAATTATAACAGAAA---TGTGTAGCATAAAATTGACCTGGCTCATCT  583

Qy   481  ATACAAGGTTACCCAGAACACCCAAAGGAGATGTATTT  540
          || |  ||||| ||||| || | ||| ||||| | | 
Db   584  ATACACGGTTACCCAGAACCTAAGGAACATGAGTGTTTTGCTAAGAACCAAGAANTCAACT  643

Qy   541  ACTAAGTATGATACTGTCATGAAGAAATCTCAAAATAAATGTCACAGAACTCTTCACAACGTT  600
          ||  ||| ||| | |||| ||||||||  || ||| || ||||| ||||||| |  || |||
Db   644  ATCGAGTGATGATGGTATTATGCAGAAANTCTCAAGATAATGCTCACAGAACTCGTACGACGTT  703

Qy   601  TCTATCAGCTTGTTCCTTCTCAGTCTCCCTGAAG---CAAGCAAGTGAGCAGCATCTTCTGTGTC  657
          ||| | |||  || | |  |||  || ||||| |   || |||  ||||||| ||| |  | | 
Db   704  TCCATCAGCTTGTTCGTTTCAATCCCTGATGTTACGGAGCAAATATGACCATCTTCTGTATT  763

Qy   658  CTGCAACTTGAGTCAATGAAAGCTTCCCTGCCCTACCTTAAATATATGACAATACGAAA  717
          ||| ||||| |  ||| | |||||||| |  |||| |  |||  || ||| | | ||||
Db   764  CTGGAAACTGACAAGACGCGGCGGTTTTATCTTCCAGCTTTGCTTTCTATAGA---GCTTGAGGAC  820

Qy   718  CCCACCCTGATGGAGACCACCATCCCTCTGGATTGCGCGGCTCTGTTGTAATTGGGTCATT  777
          ||| ||| |||  | |  |||| | || || | || | |  ||| |  ||  | |||  | 
Db   821  CCTCAGCCTGCCCCCAGACCACATTCCTTGGATTATGGAGCTGCACTGTACTTCCAA---CAGTTATT  877

Qy   778  TTGTGTGGGGATGGTGGTTCTTCTTAACACTAAGGAAA---AGGAAGAAGAAGCAGCAGCCTGGC  834
          ||||| || ||||| | ||||| |||| ||| ||||| | |||||||||||||| | | || |
Db   878  ATATGTGATGGTGTTTCTGTCTAATCCCCAGACCACAGTTTCTTATCGGAATGTCAAAGCGGCCTGC  937

Qy   835  CCCTCTCATGAATGTGAAACCAACAAAGTGGAGAAAGAAAAGAAAGTGACGGACCAAGGAA  894
          |||||||||||| || | | ||||| |||||| |||||||  |||||||| || ||||||
Db   938  AACTCTTTATAAATGTGGAACCAACACACACACAAGTGGAAGAAAGAAGTGAACAGACCAAGAA  997

Qy   895  AGAGTACGGTACCATGAAAACGGAAAGAATCTGATGAAGCCCAGTGTG---TTAACATTTCG  951
          || |||| || | |   |||| | | ||| |||| | || |  ||    ||||||||||||
Db   998  AGAGAAAAAAATCCATATACCTGAAAGATCTGATGAAGAGAAGCCCAGCGTGTTTTTAAAAGTTCG  1057

Qy   952  AAGACAGCTTCAGGCGGCGACAACAGTACTACACAGTTT  987
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RESULT 7
US-08-479-744A-2
Sequence 2, Application US/0847974A
Patent No. 6084067

; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,744A
; FILING DATE: June 7, 1995
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/280,757
; FILING DATE: 26-JUL-1994
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 28-AUG-1993
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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Qy    4 QCTMGLSNILFVWMAFLLSGAAPLKIQAYFNETADLPCQFANSQNQSLSELVVFWQDQENL 63
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Db    4 QCTMGLSNILFVWMAFLLSGAAPLKIQAYFNETADLPCQFANSQNQSLSELVVFWQDQENL 63

Qy   64 VLNEVILGKEKPDSVHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRI 123
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Qy  124 HQMNSDLSVLANFSQPEIMVTSNRTENSGIINLTCSSIQGYPEPKEMYFLVKTENSSTKY 183
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Qy  184 DTVMKKSQNNVTELYNVSISLSFSVPE-ASNVSIFCVLQLESMKLPSLPYNIDAHTKPTP 242
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RESULT 8
US-08-280-757B-2
Sequence 2, Application US/0828075 7B
Patent No. 6130316

; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; APPLICANT: Greenfield, Edward
; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/280,757B
; FILING DATE: 26-JUL-1994
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941

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Qy    4 RCTMBLNNILFVWTLLLYGAAASMKSQAYFNKTGELPCHFTNSQNISLDELVVFWQDQDKL 63
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Db    4 QCTMGLSNILFVWMAFLLSGAAPLKIQAYFNETADLPCQFANSQNQSLSELVVFWQDQENL 63

Qy   64 VLYELYRGKENPQNVHRKYKGRTSFDKDNWTLRLHNLQIKDKGLYQCFVHHKGPKGLVPM 123
        ||:|:||||||||||||||||||||:|:|||||||||||||||||||:|||| ||||||
Db   64 VLNEVILGKEKPDSVHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRI 123

Qy  124 HQMNSDLSVLANFSQPEIMVTSNRTENSGIINLTCSSIQGYPEPKEMYFLVKTENSSTKY 183
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Db  124 HQMNSELSVLANFSQPEIVPISNITENV-YINLTCSSIHGYPEPKKMSVLLRTKNSTIEY 182

Qy  184 DTVMKKSQNNVTELYNVSISLSFSVPE-ASNVSIFCVLQLESMKLPSLPYNIDAHTKPTP 242
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Db  183 DTVMKKSQNNVTELYNVSISLSFSVPE-ASNVSIFCVLQLESMKLPSLPYNIDAHTKPTP 241

Qy  243 DGDHILWIAALLVMLVILCGMVFFLTLRK-RKKKQPGPSHECETNKVERKESEQTKERVR 301
        |||||||||||:||||||||||||||||| ||||||||| :||.|.||||||||||
Db  242 PPDHIPMITAVL-PTVIICVMVFCLILMKWKKKKRPRNSYKCGTNTMEREESEQTKKREK 300

Qy  302 YHETERSDEAQCV-NISKTASGDNSTTQF 329
        ||||||||||||| |||||:||||||||:
Db  301 IHIPERSDEAQRVFKSSKTSSCDKSDTCF 329
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